

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Phenotypic information for the initial study cohort of 95 women.

File Name: Supplementary Data 2

Description: Sequencing and annotation for the study cohort of 95 women.

File Name: Supplementary Data 3

Description: List of OTUs. * Experimentally determined.

File Name: Supplementary Data 4

Description: Sequencing and annotation for the cohort of 15 additional women.

File Name: Supplementary Data 5

Description: Sequencing and annotation for the cohort of 15 additional women in different protocols.

File Name: Supplementary Data 6

Description: Signature OTUs for each site of the vagino-uterine microbiota. Based on IndVal, a well-established method in ecology considering both the occurrence and abundance of species.

File Name: Supplementary Data 7

Description: Community types of the vagino-uterine microbiota for all samples from the study cohort of 95 women.

File Name: Supplementary Data 8

Description: PERMANOVA for the influence of phenotypes on the microbiota. 9999 permutations, Bray-Curtis distance. Phenotypes with $p < 0.05$ in at least one site are shown. FDR control using the Benjamini-Hochberg procedure.

File Name: Supplementary Data 9

Description: PERMANOVA for the influence of phenotypes on the microbiota. 9999 permutations, unweighted UniFrac distance. Phenotypes with $p < 0.05$ in at least one site are shown. FDR control using the Benjamini-Hochberg procedure.

File Name: Supplementary Data 10

Description: OTUs included in the random forest classifiers for adenomyosis.

File Name: Supplementary Data 11

Description: OTUs included in the random forest classifiers for infertility and infertility due to endometriosis.